

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/578,856
Source: IFWP
Date Processed by STIC: 2/8/07

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER** **VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/578,856

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."

- 2 Invalid Line Length The rules require that a line **not exceed** 72 characters in length. This includes white spaces.

- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.

- 4 ✓ Non-ASCII The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**

- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for **each** skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped
 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If **intentional**, please insert the following lines for **each** skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000

- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.
 In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.

- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence. (see item 11 below)

- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules

- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

- 13 Misuse of n/Xaa "**n**" can **only** represent a single nucleotide; "**Xaa**" can **only** represent a single amino acid



IFWP

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/578,856

DATE: 02/09/2007

TIME: 15:25:06

Input Set : N:\AMC\PTO.AMC.txt

Output Set: N:\CRF4\02092007\J578856.raw

4 <110> APPLICANT: Vollmers, Philip
 6 <120> TITLE OF INVENTION: Human monoclonal antibody
 C--> 8 <140> CURRENT APPLICATION NUMBER: US/10/578,856
 C--> 8 <141> CURRENT FILING DATE: 2006-05-11
 W--> 0 <130> FILE REFERENCE:
 8 <150> PRIOR APPLICATION NUMBER: DE-10 353 175.0
 9 <151> PRIOR FILING DATE: 2003-11-14
 11 <160> NUMBER OF SEQ ID NOS: 4

*see item 4 on
 Error Summary
 sheet
 Does Not Comply
 Corrected Diskette Needed
 suppl, 3-4*

ERRORED SEQUENCES

13 <210> SEQ ID NO: 1
 14 <211> LENGTH: 96
 15 <212> TYPE: DNA *PRT This is not a DNA sequence*
 16 <213> ORGANISM: Homo sapiens
 18 <220> FEATURE:
 19 <223> OTHER INFORMATION: Amino acid sequence of the variable region of the light chain
 (VL) of
 20 antibody
 21 SAM-6
 23 <400> SEQUENCE: 1
 25 Ser Tyr Val Leu Thr Gln Pro Pro Ser Val Ser Val Ser Pro Gly
 26 1 5 10 15
 29 Gln Thr Ala Ser Ile Thr Cys Ser Gly Asp Lys Leu Gly Asp Lys
 30 20 25 30
 33 Tyr Ala Cys Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Val Leu
 34 35 40 45
 37 Val Ile Tyr Gln Asp Ser Lys Arg Pro Ser Gly Ile Pro Glu Arg
 38 50 55 60
 41 Phe Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser
 42 65 70 75
 45 Gly Thr Gln Ala Met Asp Glu Ala Asp Tyr Tyr Cys Gln Ala Trp
 46 80 85 90
 49 Asp Ser Ser Ile Val Val
 E--> 50 95
 113 <210> SEQ ID NO: 3
 114 <211> LENGTH: 110
 115 <212> TYPE: DNA *PRT*
 116 <213> ORGANISM: Homo sapiens
 118 <220> FEATURE:
 119 <223> OTHER INFORMATION: Amino acid sequence of the variable region of the heavy
 chain (VH) of
 120 antibody

121

SAM-6

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Input Set : N:\AMC\PTO.AMC.txt

Output Set: N:\CRF4\02092007\J578856.raw

```

123 <400> SEQUENCE: 3
125 Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly
126 1 5 10 15
129 Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
130 20 25 30
133 Ser Tyr Ala Met His Trp Val Arg Glu Ala Pro Gly Lys Gly Leu
134 35 40 45
137 Glu Trp Val Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr
138 50 55 60
141 Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser
142 65 70 75
145 Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
146 80 85 90
149 Thr Ala Val Tyr Tyr Cys Ala Arg Asp Arg Leu Ala Val Ala Gly
150 95 100 105
153 Lys Thr Phe Asp Tyr
E--> 154 110
168 <210> SEQ ID NO: 4
169 <211> LENGTH: 330
170 <212> TYPE: DNA
171 <213> ORGANISM: Homo sapiens
173 <220> FEATURE:
174 <223> OTHER INFORMATION: Nucleotide sequence of the variable region of the heavy
chain (VH) of
175 antibody
176 SAM-6
178 <400> SEQUENCE: 4
180 cag gtg cag ctg gtg gag tct ggg gga ggc gtg gtc cag cct ggg 45
181 Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly
182 1 5 10 15
185 agg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt 90
186 Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
187 20 25 30
190 agc tat gct atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg 135
191 Ser Tyr Ala Met His Trp Val Arg Glu Ala Pro Gly Lys Gly Leu
192 35 40 45
195 gag tgg gtg gca gtt ata tca tat gat gga agc aat aaa tac tac 180
196 Glu Trp Val Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr
197 50 55 60
200 gca gac tcc gtg aag ggc cga ttc acc atc tcc aga gac aat tcc 225
201 Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser
202 65 70 75
205 aag aac acg ctg tat ctg caa atg aac agc ctg aga gct gag gac 270
206 Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
207 80 85 90
210 acg gct gtg tat tac tgt gcg aga gat cgg tta gca gtg gct ggt 315
211 Thr Ala Val Tyr Tyr Cys Ala Arg Asp Arg Leu Ala Val Ala Gly
212 95 100 105
E--> 215 aaa act ttt gac tac
216 Lys Thr Phe Asp Tyr

```

330 ← insert

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/578,856

DATE: 02/09/2007

TIME: 15:25:06

Input Set : N:\AMC\PTO.AMC.txt

Output Set: N:\CRF4\02092007\J578856.raw

W--> 217

110

Per 1.823 of Sequence Rules, a
fixed-width font should be
used throughout the Sequence
Listing. Do not use bold print,
either. Do not use format markers.

VERIFICATION SUMMARY

DATE: 02/09/2007

PATENT APPLICATION: US/10/578,856

TIME: 15:25:07

Input Set : N:\AMC\PTO.AMC.txt

Output Set: N:\CRF4\02092007\J578856.raw

L:8 M:270 C: Current Application Number differs, Replaced Current Application No
L:8 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:0 M:201 W: Mandatory field data missing, <130> FILE REFERENCE
L:50 M:301 E: (44) No Sequence Data was Shown, SEQ ID:1
L:50 M:252 E: No. of Seq. differs, <211> LENGTH:Input:96 Found:0 SEQ:1
L:154 M:301 E: (44) No Sequence Data was Shown, SEQ ID:3
L:154 M:252 E: No. of Seq. differs, <211> LENGTH:Input:110 Found:0 SEQ:3
L:215 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:330 SEQ:4
L:217 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4